Sample Submission Guidelines

General guidelines

- Please provide an Excel file containing the current sample list and sample concentrations electronically. Please also include a printed copy of the sample list with the shipment.
- Please use short and unambiguous sample names. Avoid complex multi-word names (e.g. *Leukemic B cells MU1630 2118*) and purely numerical sample names (e.g. *1, 2, 3*).
- Samples should preferably be provided in 1.5 mL tubes or PCR plates. Do not submit samples in individual PCR tubes.
- If you have already performed quality control (QC) of your samples (e.g. using agarose gel electrophoresis, Bioanalyzer, or Fragment Analyzer), please provide the corresponding QC reports.

RNA/DNA for QC

- Known concentration: 4 µL per sample.
- Unknown concentration: 8 µL per sample.

RNA for library preparation

- Recommended amount: 100 ng/µL in 20 µL.
- Minimum total amount: 500 ng.
- Minimum volume: 20 ul.
- Please normalize all samples to the same concentration.
- Samples should be shipped on sufficient dry ice to ensure that they remain frozen throughout transport.
- RNA should be intact, with an RIN ≥ 7.0, and free of genomic DNA contamination (DNase-treated).

DNA for library preparation

- Recommended amount: 50 ng/µL in 20 µL.
- Minimum total amount: 100 ng.
- Minimum volume: 20 ul.
- Please normalize all samples to the same concentration.
- Samples should be shipped on cooling packs.

Sequencing libraries

- Pooled libraries are preferred, with a minimum concentration of 5 nM and a minimum volume of 20 µL. Individual libraries can also be submitted.
- Samples should be shipped on cooling packs.
- Please fill in the sample sheet with the sample names and index sequences on our website http://cfb.ceitec.muni.cz/sequia/
- If you do not have access to the website yet, a registration link will be sent to you.
- Sample names must contain only letters, numbers, underscores (_), and dashes (-). Spaces and other special characters are not allowed.